PCT10

RAW SEQUENCE LISTING   DATE: 07/30/2003
PATENT APPLICATION: US/10/089,147   TIME: 18:04:56

     Input Set : A:\089147sq
     Output Set: N:\CRF4\07302003\J089147.raw

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 3 <110> APPLICANT: Kindl, Helmut
 4         May, Christian
 5         Feussner, Ivo
 7 <120> TITLE OF INVENTION: The N-terminal beta-barrel structure of lipid body
lipoxygenase mediates
 8         its binding to liposomes and lipid bodies
10 <130> FILE REFERENCE: 99_1235
12 <140> CURRENT APPLICATION NUMBER: US 10/089,147
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C--> 13 **<141> CURRENT FILING DATE: 2002-03-27**
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15 <150> PRIOR APPLICATION NUMBER: PCT/EP/00/09912
16 <151> PRIOR FILING DATE: 2000-10-10
18 <160> NUMBER OF SEQ ID NOS: 4
20 <170> SOFTWARE: WordPerfect 6.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 732
24 <212> TYPE: DNA
25 <213> ORGANISM: Cucumis sativus
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)..(732)
31 <400> SEQUENCE: 1
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ENTERED

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35 Met Phe Gly Ile Gly Lys Asn Ile Ile Glu Gly Ala Leu Asn Thr Thr
36  1               5                   10                  15
38 gga gat ctt gca ggt tct gtt atc aat gct ggt ggt aac att tta gat   96
39 Gly Asp Leu Ala Gly Ser Val Ile Asn Ala Gly Gly Asn Ile Leu Asp
40              20                  25                  30
42 aga gtt tcc agt ctt gga gga aac aaa atc aaa ggg aaa gtg att ctt  144
43 Arg Val Ser Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu
44          35                  40                  45
46 atg aga agc aat gtt ttg gat ttc act gaa ttt cat tcc aat ctt ctt  192
47 Met Arg Ser Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu
48      50                  55                  60
50 gat aac ttc act gag ctc ttg ggt ggt ggt gtt tct ttc caa ctc att  240
51 Asp Asn Phe Thr Glu Leu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile
52  65                  70                  75                  80
54 agt gcc act cat act tca aat gac tca aga ggg aaa gtt ggg aac aag  288
55 Ser Ala Thr His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys
56                  85                  90                  95
58 gca tat ttg gag agg tgg cta act tca atc cca cca ctg ttt gct gga  336
59 Ala Tyr Leu Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly
60              100                 105                 110
62 gaa tca gtg ttc caa atc aac ttt caa tgg gat gaa aat ttt gga ttt  384
63 Glu Ser Val Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe
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64        115                  120                  125
66 cca gga gct ttc ttc ata aaa aat gga cat aca agt gaa ttc ttt ctc   432
67 Pro Gly Ala Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu
68    130                  135                  140
70 aaa tct ctc act ctt gat gat gtt cct ggc tat ggc aga gtc cat ttt   480
71 Lys Ser Leu Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe
72 145                  150                  155                  160
74 gat tgc aat tct tgg gtt tac cct tct gga aga tac aag aaa gat cgc   528
75 Asp Cys Asn Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg
76                  165                  170                  175
78 att ttc ttt gcc aat cat gtt tat ctt cca agt caa aca cca aac cct   576
79 Ile Phe Phe Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro
80                  180                  185                  190
82 ctt cgt aag tat aga gag gaa gaa ttg tgg aat ttg aga gga gat gga   624
83 Leu Arg Lys Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly
84        195                  200                  205
86 aca gga gaa aga aag gaa tgg gat aga att tat gac tat gat gtt tat   672
87 Thr Gly Glu Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr
88    210                  215                  220
90 aat gac att gct gac cct gat gtt ggt gat cat cgt cct att ctc ggt.   720
91 Asn Asp Ile Ala Asp Pro Asp Val Gly Asp His Arg Pro Ile Leu Gly
92 225                  230                  235                  240
94 ggg acg acc gaa                                                    732
95 Gly Thr Thr Glu
98 <210> SEQ ID NO: 2
99 <211> LENGTH: 244
100 <212> TYPE: PRT
101 <213> ORGANISM: Cucumis sativus
103 <400> SEQUENCE: 2
105 Met Phe Gly Ile Gly Lys Asn Ile Ile Glu Gly Ala Leu Asn Thr Thr
106  1               5                  10                  15
108 Gly Asp Leu Ala Gly Ser Val Ile Asn Ala Gly Gly Asn Ile Leu Asp
109              20                  25                  30
111 Arg Val Ser Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu
112           35                  40                  45
114 Met Arg Ser Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu
115       50                  55                  60
117 Asp Asn Phe Thr Glu Leu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile
118  65                  70                  75                  80
120 Ser Ala Thr His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys
121              85                  90                  95
123 Ala Tyr Leu Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly
124              100                  105                  110
126 Glu Ser Val Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe
127           115                  120                  125
129 Pro Gly Ala Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu
130       130                  135                  140
132 Lys Ser Leu Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe
133 145                  150                  155                  160
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135 Asp Cys Asn Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg
136                 165             170             175
138 Ile Phe Phe Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro
139                 180             185             190
141 Leu Arg Lys Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly
142             195             200             205
144 Thr Gly Glu Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr
145         210             215             220
147 Asn Asp Ile Ala Asp Pro Asp Val Gly Asp His Arg Pro Ile Leu Gly
148 225                 230             235             240
150 Gly Thr Thr Glu
152 <210> SEQ ID NO: 3
153 <211> LENGTH: 2964
154 <212> TYPE: DNA
155 <213> ORGANISM: Cucumis sativus
157 <220> FEATURE:
158 <221> NAME/KEY: CDS
159 <222> LOCATION: (48)..(2684)
161 <400> SEQUENCE: 3
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164                                                     Met Phe Gly
165                                                     1
167 att ggg aag aac atc att gaa ggg gcc ttg aat aca act gga gat ctt  104
168 Ile Gly Lys Asn Ile Ile Glu Gly Ala Leu Asn Thr Thr Gly Asp Leu
169         5                   10                  15
171 gca ggt tct gtt atc aat gct ggt ggt aac att tta gat aga gtt tcc  152
172 Ala Gly Ser Val Ile Asn Ala Gly Gly Asn Ile Leu Asp Arg Val Ser
173 20                  25                  30                  35
175 agt ctt gga gga aac aaa atc aaa ggg aaa gtg att ctt atg aga agc  200
176 Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu Met Arg Ser
177                     40                  45                  50
179 aat gtt ttg gat ttc act gaa ttt cat tcc aat ctt ctt gat aac ttc  248
180 Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu Asp Asn Phe
181             55                  60                  65
183 act gag ctc ttg ggt ggt ggt gtt tct ttc caa ctc att agt gcc act  296
184 Thr Glu Leu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile Ser Ala Thr
185             70                  75                  80
187 cat act tca aat gac tca aga ggg aaa gtt ggg aac aag gca tat ttg  344
188 His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys Ala Tyr Leu
189         85                  90                  95
191 gag agg tgg cta act tca atc cca cca ctg ttt gct gga gaa tca gtg  392
192 Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly Glu Ser Val
193 100                 105                 110                 115
195 ttc caa atc aac ttt caa tgg gat gaa aat ttt gga ttt cca gga gct  440
196 Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe Pro Gly Ala
197                 120                 125                 130
199 ttc ttc ata aaa aat gga cat aca agt gaa ttc ttt ctc aaa tct ctc  488
200 Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu Lys Ser Leu
201             135                 140                 145
```

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203 act ctt gat gat gtt cct ggc tat ggc aga gtc cat ttt gat tgc aat    536
204 Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe Asp Cys Asn
205         150             155                 160
207 tct tgg gtt tac cct tct gga aga tac aag aaa gat cgc att ttc ttt    584
208 Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg Ile Phe Phe
209     165             170                 175
211 gcc aat cat gtt tat ctt cca agt caa aca cca aac cct ctt cgt aag    632
212 Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro Leu Arg Lys
213 180             185                 190                 195
215 tat aga gag gaa gaa ttg tgg aat ttg aga gga gat gga aca gga gaa    680
216 Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly Thr Gly Glu
217             200             205                 210
219 aga aag gaa tgg gat aga att tat gac tat gat gtt tat aat gac att    728
220 Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr Asn Asp Ile
221             215             220                 225
223 gct gac cct gat gtt ggt gat cat cgt cct att ctc ggt ggg acg acc    776
224 Ala Asp Pro Asp Val Gly Asp His Arg Pro Ile Leu Gly Gly Thr Thr
225         230             235                 240
227 gaa tat cct tac cct cgt agg gga aga aca gga cga cca cga tca aga    824
228 Glu Tyr Pro Tyr Pro Arg Arg Gly Arg Thr Gly Arg Pro Arg Ser Arg
229     245             250                 255
231 aga gac cac aat tat gag agc aga ttg tca cca ata atg agc tta gac    872
232 Arg Asp His Asn Tyr Glu Ser Arg Leu Ser Pro Ile Met Ser Leu Asp
233 260             265                 270                 275
235 atc tat gta cca aaa gat gaa aac ttt ggg cat ttg aag atg tca gat    920
236 Ile Tyr Val Pro Lys Asp Glu Asn Phe Gly His Leu Lys Met Ser Asp
237             280             285                 290
239 ttc ctt ggt tat aca tta aaa gca ctt tcg ata tca atc aaa cca gga    968
240 Phe Leu Gly Tyr Thr Leu Lys Ala Leu Ser Ile Ser Ile Lys Pro Gly
241             295             300                 305
243 ctt caa tcc ata ttt gat gta act cca aat gaa ttt gac aat ttt aaa   1016
244 Leu Gln Ser Ile Phe Asp Val Thr Pro Asn Glu Phe Asp Asn Phe Lys
245         310             315                 320
247 gaa gtt gat aat ctc ttt gag aga ggt ttt ccc att cca ttt aat gct   1064
248 Glu Val Asp Asn Leu Phe Glu Arg Gly Phe Pro Ile Pro Phe Asn Ala
249     325             330                 335
251 ttt aag acc ctc act gag gac ctc act cca cct ttg ttc aaa gca ctc   1112
252 Phe Lys Thr Leu Thr Glu Asp Leu Thr Pro Pro Leu Phe Lys Ala Leu
253 340             345                 350                 355
255 gtg agg aat gat ggt gaa aaa ttc ctc aaa ttt cct act ccc gaa gtt   1160
256 Val Arg Asn Asp Gly Glu Lys Phe Leu Lys Phe Pro Thr Pro Glu Val
257             360             365                 370
259 gtc aaa gat aat aaa ata gga tgg agc act gat gaa gaa ttt gca aga   1208
260 Val Lys Asp Asn Lys Ile Gly Trp Ser Thr Asp Glu Glu Phe Ala Arg
261             375             380                 385
263 gaa atg tta gca gga ccc aat cct cta ttg att cgt cgt ctt gaa gct   1256
264 Glu Met Leu Ala Gly Pro Asn Pro Leu Leu Ile Arg Arg Leu Glu Ala
265         390             395                 400
267 ttt cca cca aca agt aag ctt gac cca aat gtt tat ggg aat caa aac   1304
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Input Set : A:\089147sq
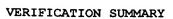Output Set: N:\CRF4\07302003\J089147.raw

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268 Phe Pro Pro Thr Ser Lys Leu Asp Pro Asn Val Tyr Gly Asn Gln Asn
269     405             410             415
271 agt acc atc act gaa gaa cac ata aag cat ggt tta gat ggt ctt acg   1352
272 Ser Thr Ile Thr Glu Glu His Ile Lys His Gly Leu Asp Gly Leu Thr
273 420             425             430                 435
275 gtt gat gag gca atg aag caa aac agg ctc tac ata gtg gat ttc cat   1400
276 Val Asp Glu Ala Met Lys Gln Asn Arg Leu Tyr Ile Val Asp Phe His
277             440             445             450
279 gat gca tta atg ccc tat ctt aca agg atg aat gca aca tca aca aaa   1448
280 Asp Ala Leu Met Pro Tyr Leu Thr Arg Met Asn Ala Thr Ser Thr Lys
281             455             460             465
283 aca tat gcc aca aga aca ttg ctt ctt ttg aaa gat gat ggg act ttg   1496
284 Thr Tyr Ala Thr Arg Thr Leu Leu Leu Leu Lys Asp Asp Gly Thr Leu
285             470             475             480
287 aag cca ttg gtt att gag tta gcc ttg cca cat cct caa gga gat caa   1544
288 Lys Pro Leu Val Ile Glu Leu Ala Leu Pro His Pro Gln Gly Asp Gln
289 485             490             495
291 ctt ggt gcc att agc aaa cta tac ttt cca gct gaa aat gga gtt caa   1592
292 Leu Gly Ala Ile Ser Lys Leu Tyr Phe Pro Ala Glu Asn Gly Val Gln
293 500             505             510             515
295 aaa tcc att tgg caa ttg gct aaa gct tat gta act gtt aat gat gtt   1640
296 Lys Ser Ile Trp Gln Leu Ala Lys Ala Tyr Val Thr Val Asn Asp Val
297             520             525             530
299 ggc tac cat caa ctt att agt cat tgg ttg cat act cat gct gta ctt   1688
300 Gly Tyr His Gln Leu Ile Ser His Trp Leu His Thr His Ala Val Leu
301             535             540             545
303 gag cca ttt gtg att gca aca cat aga caa ttg agc gtg ctt cat cca   1736
304 Glu Pro Phe Val Ile Ala Thr His Arg Gln Leu Ser Val Leu His Pro
305             550             555             560
307 atc cat aag ttg ctt gtt cct cat tac aaa gac act atg ttt ata aat   1784
308 Ile His Lys Leu Leu Val Pro His Tyr Lys Asp Thr Met Phe Ile Asn
309     565             570             575
311 gca tct gca aga caa gtt ttg atc aat gcc aat ggt ctt atc gaa aca   1832
312 Ala Ser Ala Arg Gln Val Leu Ile Asn Ala Asn Gly Leu Ile Glu Thr
313 580             585             590             595
315 acc cat tat cca tca aaa tat tca atg gag ttg tca tct atc ttg tac   1880
316 Thr His Tyr Pro Ser Lys Tyr Ser Met Glu Leu Ser Ser Ile Leu Tyr
317             600             605             610
319 aag gat tgg acc ttc cct gat caa gca tta cct aat aat ctc atg aag   1928
320 Lys Asp Trp Thr Phe Pro Asp Gln Ala Leu Pro Asn Asn Leu Met Lys
321             615             620             625
323 aga gga cta gct gtg gag gac tca agt gcc ccc cat gga ctt aga ttg   1976
324 Arg Gly Leu Ala Val Glu Asp Ser Ser Ala Pro His Gly Leu Arg Leu
325             630             635             640
327 cta ata aat gat tat cca ttt gct gtt gat ggt ctt gac att tgg tca   2024
328 Leu Ile Asn Asp Tyr Pro Phe Ala Val Asp Gly Leu Asp Ile Trp Ser
329             645             650             655
331 gcc att aaa aca tgg gta cag gat tat tgc tgt ctc tac tac aaa gat   2072
332 Ala Ile Lys Thr Trp Val Gln Asp Tyr Cys Cys Leu Tyr Tyr Lys Asp
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VERIFICATION SUMMARY   DATE: 07/30/2003
PATENT APPLICATION: **US/10/089,147**   TIME: 18:04:57

Input Set : **A:\089147sq**
Output Set: **N:\CRF4\07302003\J089147.raw**

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date